

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/560,378
Source: P4/10
Date Processed by STIC: 12/20/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/560,378

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics**
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino**
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0**
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences**
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences**
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's**
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>**
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0**
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



Suggestion: Consult Sequence Rules for guidance IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/560,378

DATE: 12/20/2005

TIME: 11:25:31

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\12202005\J560378.raw

2 <110> APPLICANT: Daiichi Asubio Pharma Co., Ltd.

W--> 3 <120> TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR PREVENTING OR TREATING

W--> 4 Th1-MEDIATED IMMUNE DISEASES

W--> 5 <130> FILE REFERENCE: 031317

C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/560,378

C--> 6 <141> CURRENT FILING DATE: 2005-12-13

W--> 6 <160> NUMBER OF SEQ ID: 16

*see item 4 on
Err summary sheet*

see pp 1-4

ERRORED SEQUENCES

89 <210> SEQ ID NO: 9

90 <211> LENGTH: 21

91 <212> TYPE: DNA

92 <213> ORGANISM: Artificial Sequence

W--> 93 <220> FEATURE:

W--> 93 <223> OTHER INFORMATION:

W--> 93 <400> SEQUENCE: 9

E--> 94 gggaacctca agtcatccaa c

96 <210> SEQ ID NO: 10

97 <211> LENGTH: 20

98 <212> TYPE: DNA

99 <213> ORGANISM: Artificial Sequence

W--> 100 <220> FEATURE:

W--> 100 <223> OTHER INFORMATION:

W--> 100 <400> SEQUENCE: 10

E--> 101 atgaagggca aaggcaaggt

103 <210> SEQ ID NO: 11

104 <211> LENGTH: 20

105 <212> TYPE: DNA

106 <213> ORGANISM: Artificial Sequence

W--> 107 <220> FEATURE:

W--> 107 <223> OTHER INFORMATION:

W--> 107 <400> SEQUENCE: 11

E--> 108 tctagaaaat gacagcatca

110 <210> SEQ ID NO: 12

111 <211> LENGTH: 20

112 <212> TYPE: DNA

113 <213> ORGANISM: Artificial Sequence

W--> 114 <220> FEATURE:

W--> 114 <223> OTHER INFORMATION:

W--> 114 <400> SEQUENCE: 12

E--> 115 tgacaacttt gatgtctaca

*Does Not Comply
Corrected Diskette Needed*

*see p. 3 for error explanation
21 ← insert cumulative nucleotide total
at right margin
of each line*

same error

20 ← insert

same

20 ←

same

20 ←

RAW SEQUENCE LISTING

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\12202005\J560378.raw

117 <210> SEQ ID NO: 13
118 <211> LENGTH: 24
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
W--> 121 <220> FEATURE:
W--> 121 <223> OTHER INFORMATION: *same*
W--> 121 <400> SEQUENCE: 13
E--> 122 gaaggtatcg ccgggcaggt gtcc 24 ←
124 <210> SEQ ID NO: 14
125 <211> LENGTH: 24
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
W--> 128 <220> FEATURE: *same*
W--> 128 <223> OTHER INFORMATION:
W--> 128 <400> SEQUENCE: 14
E--> 129 tcttcccga attcccgatg tttt 24 ←
131 <210> SEQ ID NO: 15
132 <211> LENGTH: 21
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
W--> 135 <220> FEATURE: *same*
W--> 135 <223> OTHER INFORMATION:
W--> 135 <400> SEQUENCE: 15 21 ←
E--> 136 tcctgtggca tccacgaaac t
138 <210> SEQ ID NO: 16
139 <211> LENGTH: 21
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence
W--> 143 <220> FEATURE:
W--> 143 <223> OTHER INFORMATION:
W--> 143 <400> SEQUENCE: 16
E--> 144 gaagcatttg cgggtggacga t 21 ←
E--> 145 1
E--> 147 1 *delete*

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\pto.da.txt
Output Set: N:\CRF4\12202005\J560378.raw

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:9,10,11,12,13,14,15,16

10/560,378

4

do NOT use brackets
[Sequence Listing]

SEQUENCE LISTING

(all upper-case letters)

<110> Daiichi Asubio Pharma Co., Ltd.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/560,378

DATE: 12/20/2005

TIME: 11:25:32

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\12202005\J560378.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
 L:5 M:283 W: Missing Blank Line separator, <130> field identifier
 L:6 M:270 C: Current Application Number differs, Replaced Current Application No
 L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:6 M:283 W: Missing Blank Line separator, <160> field identifier
 L:12 M:283 W: Missing Blank Line separator, <400> field identifier
 L:22 M:283 W: Missing Blank Line separator, <400> field identifier
 L:32 M:283 W: Missing Blank Line separator, <400> field identifier
 L:41 M:283 W: Missing Blank Line separator, <400> field identifier
 L:51 M:283 W: Missing Blank Line separator, <400> field identifier
 L:61 M:283 W: Missing Blank Line separator, <400> field identifier
 L:71 M:283 W: Missing Blank Line separator, <400> field identifier
 L:83 M:283 W: Missing Blank Line separator, <400> field identifier
 L:93 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
 ORGANISM:Artificial Sequence
 L:93 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
 ORGANISM:Artificial Sequence
 L:93 M:283 W: Missing Blank Line separator, <400> field identifier
 L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:93
 L:94 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:9
 L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
 ORGANISM:Artificial Sequence
 L:100 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
 ORGANISM:Artificial Sequence
 L:100 M:283 W: Missing Blank Line separator, <400> field identifier
 L:100 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:100
 L:101 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:10
 L:107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
 ORGANISM:Artificial Sequence
 L:107 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
 ORGANISM:Artificial Sequence
 L:107 M:283 W: Missing Blank Line separator, <400> field identifier
 L:107 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:107
 L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:11
 L:114 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
 ORGANISM:Artificial Sequence
 L:114 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
 ORGANISM:Artificial Sequence
 L:114 M:283 W: Missing Blank Line separator, <400> field identifier
 L:114 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:114
 L:115 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
 L:121 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
 ORGANISM:Artificial Sequence
 L:121 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
 ORGANISM:Artificial Sequence
 L:121 M:283 W: Missing Blank Line separator, <400> field identifier
 L:121 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:121
 L:122 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:13
 L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
 ORGANISM:Artificial Sequence
 L:128 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
 ORGANISM:Artificial Sequence
 L:128 M:283 W: Missing Blank Line separator, <400> field identifier

L:128 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:128
L:129 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:14
L:135 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:135 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:135 M:283 W: Missing Blank Line separator, <400> field identifier
L:135 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:135
L:136 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:15

VERIFICATION SUMMARY

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\12202005\J560378.raw

L:143 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:143 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:143 M:283 W: Missing Blank Line separator, <400> field identifier
L:143 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:143
L:144 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:16
L:145 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:147 M:254 E: No. of Bases conflict, this line has no nucleotides.